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Interactive comment on “Soil organic carbon (SOC) accumulation in rice paddies under long-term agro-ecosystem experiments in southern China – VI. Changes in microbial community structure and respiratory activity” by D. Liu et al.

Anonymous Referee #2

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This study addresses the effects different fertilization treatments in rice argoecosystems in China on soil microbial communities and SOC, specifically linking changes in microbial community dominance and function in storing soil C. This work is timely and helps increase our understanding of the linkages between microbial communities and soil carbon dynamics. It also sheds light on these processes in agroecosystems, which are extensive and important, though often overlooked in scientific literature. However, much of the context for the work, as well as the methods, results, and discussion of

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findings, were difficult to understand due to a general language barrier. Before this work can be fully evaluated for its scientific merit, it could greatly benefit from heavy editorial assistance from a native English speaker.

While I believe the data collected are interesting and informative, there are several ways in which to improve the overall quality of this manuscript. In the introduction, the authors need to re-frame the purpose of the work and more specifically state that they are interested in linking changes in microbial community composition (specifically, bacterial versus fungal dominance) with changes in soil organic matter (aka carbon storage) across the existing infrastructure of long-term fertilization experiments. In my opinion, one of the biggest strengths (and maybe also shortcoming) of the work is that it is done in several long-term field experiments. While the authors are missing information about shorter-term mechanisms of changes in microbial communities, they are able to show the effects after 20 years of fertilization and cultivation. This indeed is rare in ecological studies and should be highlighted as the strength of the work. The discussion must also address this aspect – lack of short-term mechanisms, but evidence for how things change after 20 years.

In the methods section, there is no need to mention that the data were processed with Excel and that means and standard deviations were calculated, unless this was the only way the data were analyzed. The stepwise regression analysis does not seem like the appropriate analysis to perform on the data if the only groups being compared are treated versus control. An ANOVA or t-test is the most fitting analysis. “Polluted” means fertilized?

Overall, the results section needs to be re-done to bring in specific results rather than mentioning which table they can be found in. Some of these specifics can actually be found in the discussion section, which is not the appropriate place for these results.

Most of the results are not discussed and all need to be integrated to address the research question. Another missed opportunity is the lack of more thorough discussion

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(either in the results or discussion section) of the differences found among the different fertilization treatments. Why would we expect different fertilization treatments to affect microbial community composition and SOC differently? What aspects of the compound fertilization treatment help explain the differences in microbial community composition, fungal dominance, and C and N biomass?

Tables and Figures Table 1 – “trials” should be “experiments”. What is a rice-rape crop rotation? Rape seed? Table 3 – “Clony” should be “colony” and population is not what was being measured. “Fugal” should be “fungal” and under different fertilization treatments across three experimental sites. It would be helpful to define the fertilization treatments in the table caption here to help readers and not necessitate flipping back to other sections of the paper. Figure 2 – “blank” blocks should be “white” or “open”. Were these 8-11am measurements integrated to get one respiration #? Or averaged across sampling times and replicates? Figure 3 – y-axis label should state “Fungal:Bacterial abundance (CFU/g soil). And again, I am not sure population is what was being measured with colony counts. Center the SOC x-axis label. Figure 4 – this figure is showing the correlation of microbial C and N with SOC. Don’t need to state that this is an increase, state this in the results and discussion.

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